

SEQUENCE LISTING

<110> Chiaur, D.
Pagano, M.
Latres, E.

<120> NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS

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<141> 1999-08-27

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<151> 1998-08-28

<150> 60/118,568

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<170> PatentIn Ver. 2.0

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<212> PRT

<213> Homo sapiens

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 Glu Thr Leu Leu Lys Arg Asp Phe Leu Lys Leu Leu Pro Leu Glu Leu
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 65 70 75 80
 Cys Leu Val Ser Lys Gln Trp Asn Lys Val Ile Ser Ala Cys Thr Glu
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Lys Tyr Leu Pro Leu Leu Asp Arg Ala His Ala Ser Gln Val Cys Arg
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Asn Trp Asn Gln Val Phe His Met Pro Asp Leu Trp Arg Cys Phe Glu
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Phe Glu Leu Asn Gln Pro Ala Thr Ser Tyr Leu Lys Ala Thr His Pro
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Glu Leu Ile Lys Gln Ile Ile Lys Arg His Ser Asn His Leu Gln Tyr
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Val Ser Phe Lys Val Asp Ser Ser Lys Glu Ser Ala Glu Ala Ala Cys
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Cys	Glu	Val	Ser	Cys	Ser	Ala	Phe	Val	Glu	Phe	Val	Lys	Met	Cys	Gly	370	375	380	
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Gln	Lys	Tyr	Ser	Leu	Glu	Gln	Ile	His	Trp	Glu	Val	Ser	Lys	His	Leu	405	410		415
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<212> DNA

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Arg Glu Glu Val Asp Glu Ala Ala Ser Thr Leu Thr Arg Leu Pro Ile
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Asp Val Gln Leu Tyr Ile Leu Ser Phe Leu Ser Pro His Asp Leu Cys
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Gln Leu Gly Ser Thr Asn His Tyr Trp Asn Glu Thr Val Arg Asn Pro
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Val Asp Trp Lys Ser Leu Pro Tyr Leu Gln Ile Leu Lys Lys Pro Ile
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 210 215 220
 Leu Asn Asn Gln His Lys Phe Asn Ile Leu Ile Leu Tyr Ser Thr Thr
 225 230 235 240
 Arg Lys Glu Arg Asp Arg Ala Arg Glu Glu His Thr Ser Ala Val Asn
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 Lys Met Phe Ser Arg His Asn Glu Gly Asp Asp Arg Pro Gly Ser Arg
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 Asp Glu Phe Ser His Ile Met Ala Met Thr Asp Pro Ala Phe Gly Ser
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<400> 13

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<212> PRT

<213> Homo sapiens

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Leu Ile Cys Leu Ile Leu His Asp Asp Ile Pro Pro Pro Asn Ile Pro
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Ser Ser Thr Asp Ser Glu His Ser Ser Leu Gln Asn Asn Glu Gln Pro
      50                      55                      60

Ser Leu Ala Thr Ser Ser Asn Gln Thr Ser Ile Gln Asp Glu Gln Pro
      65                      70                      75                      80

Ser Asp Ser Phe Gln Gly Gln Ala Ala Gln Ser Gly Val Trp Asn Asp
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Asp Ser Met Leu Gly Pro Ser Gln Asn Phe Glu Ala Glu Ser Ile Gln
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Asp Asn Ala His Met Ala Glu Gly Thr Gly Phe Tyr Pro Ser Glu Pro

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<213> Homo sapiens

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Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu Asp Arg Ala Cys
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130 135 140
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Pro Lys Met Ser Ser Cys Pro His Val Ser Ser Asp Gly Ile Leu Cys
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Ala Leu Gly Leu Ser Lys Cys Glu Val Ser Cys Ser Ala Phe Ile Arg
370 375 380

Phe Val Arg Leu Cys Glu Arg Arg Leu Thr Gln Leu Ser Val Met Glu
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<210> 26
 <211> 634
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 26

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35 40 45
Leu Gly Thr Ser Ser Arg Leu Ser His Phe Pro Phe Gly Lys Ser Pro
50 55 60
Pro Arg Gly Gln Phe Val Ala Ala Ala Val Glu Ile Ala Gly Arg Ser
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Leu Gln Gln Glu Gly Tyr Ser Glu Gln Gly Tyr Leu Thr Arg Glu Gln
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Ser Arg Arg Met Ala Ala Ser Asn Ile Ser Asn Thr Asn His Arg Lys
115 120 125
Gln Val Gln Gly Gly Ile Asp Ile Tyr His Leu Leu Lys Ala Arg Lys
130 135 140
Ser Lys Glu Gln Glu Gly Phe Ile Asn Leu Glu Met Leu Pro Pro Glu
145 150 155 160
Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr Asp Leu Cys Leu
165 170 175
Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu Leu Leu Trp Gln
180 185 190
Gly Leu Cys Lys Ser Thr Trp Gly His Cys Ser Ile Tyr Asn Lys Asn
195 200 205
Pro Pro Leu Gly Phe Ser Phe Arg Lys Xaa Tyr Met Gln Leu Asp Glu
210 215 220
Gly Ser Leu Thr Phe Asn Ala Asn Pro Asp Glu Gly Val Asn Tyr Phe
225 230 235 240
Met Ser Lys Gly Ile Leu Asp Asp Ser Pro Lys Glu Ile Ala Lys Phe
245 250 255
Ile Phe Cys Thr Arg Thr Leu Asn Trp Lys Lys Leu Arg Ile Tyr Leu
260 265 270
Asp Glu Arg Arg Asp Val Leu Asp Asp Leu Val Thr Leu His Asn Phe
275 280 285
Arg Asn Gln Phe Leu Pro Asn Ala Leu Arg Glu Phe Phe Arg His Ile
290 295 300
His Ala Pro Glu Glu Arg Gly Glu Tyr Leu Glu Thr Leu Ile Thr Lys

305		310		315		320
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Leu Ser Ile Asp Leu Thr Ser Pro His Val Lys Asn Lys Met Ser Lys						
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Arg Glu Phe Ile Arg Asn Thr Arg Arg Ala Ala Gln Asn Ile Ser Glu						
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Asp Phe Val Gly His Leu Tyr Asp Asn Ile Tyr Leu Ile Gly His Val						
	385		390			395
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Ala Thr Gln Gly Leu Ser Arg Tyr Gly Gly Tyr Ile Ser Ala Gly His						
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Cys Ser Leu Ser Ile Gln Ser Ser Phe Ser Val Gln Pro Phe Phe Leu						
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Leu Pro Phe Ser Ile Leu Val Ile Ser Leu Gly Asn Ile Ile Leu Gln						
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Asn Phe Ser Phe Cys Leu Ser Arg Phe Ala Gln Ser Arg Ala Thr Val						
	465		470			475
His Ser Cys Arg Met Ile Asn His Tyr Thr Leu Lys Asp Gly Val Phe						
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Val His Ile Cys Leu Lys Asn Phe Ile His Phe His Ser Leu Tyr Lys						
	500		505			510
Tyr His Val Met Cys Thr Tyr Leu Thr Lys Glu Ile Tyr Ser His Asn						
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Tyr Phe Ile Val Lys Ile Leu Thr Lys Val Phe Pro Phe Leu Ser Asn						
	530		535			540
Val Leu Lys Phe Ile Phe Ser Glu Thr Ile Val Xaa Val Lys Val Arg						
	545		550			555
Ser Asp Phe Arg Gln Lys Pro Ile Pro Ala Ser Phe Ser Phe Lys Leu						
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Arg Val Leu Ile Cys Tyr Tyr Ile Thr Met Gln Asn Trp Gln Leu Phe						
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Leu Tyr Lys Phe Ile Ile Phe Phe Ile Leu Lys Thr Gly Leu Ile Lys						
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<210> 27
 <211> 4168
 <212> DNA
 <213> Homo sapiens

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<400> 27
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<210> 28

<211> 621

<212> PRT

<213> Homo sapiens

<400> 28

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Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
      35                      40                      45

Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
      50                      55                      60

Leu Cys Gln Ser Ser Gly Lys Val Trp Lys Glu Gln Phe Arg Val Arg
      65                      70                      75                      80

Trp Pro Ser Leu Met Lys His Tyr Ser Pro Thr Asp Tyr Val Asn Trp
      85                      90                      95

Leu Glu Glu Tyr Lys Val Arg Gln Lys Ala Gly Leu Glu Ala Arg Lys
      100                      105                      110

Ile Val Ala Ser Phe Ser Lys Arg Phe Phe Ser Glu His Val Pro Cys
      115                      120                      125

Asn Gly Phe Ser Asp Ile Glu Asn Leu Glu Gly Pro Glu Ile Phe Phe
      130                      135                      140

Glu Asp Glu Leu Val Cys Ile Leu Asn Met Glu Gly Arg Lys Ala Leu
      145                      150                      155                      160

Thr Trp Lys Tyr Tyr Ala Lys Lys Ile Leu Tyr Tyr Leu Arg Gln Gln
      165                      170                      175

Lys Ile Leu Asn Asn Leu Lys Ala Phe Leu Gln Gln Pro Asp Asp Tyr
      180                      185                      190

Glu Ser Tyr Leu Glu Gly Ala Val Tyr Ile Asp Gln Tyr Cys Asn Pro

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195					200					205					
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210					215					220					
Val	Glu	Leu	Val	Cys	Lys	Thr	Leu	Arg	Gly	Ile	Asn	Ser	Arg	His	Pro
225					230					235					240
Ser	Leu	Ala	Phe	Lys	Ala	Gly	Glu	Ser	Ser	Met	Ile	Met	Glu	Ile	Glu
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Leu	Gln	Ser	Gln	Val	Leu	Asp	Ala	Met	Asn	Tyr	Val	Leu	Tyr	Asp	Gln
			260					265					270		
Leu	Lys	Phe	Lys	Gly	Asn	Arg	Met	Asp	Tyr	Tyr	Asn	Ala	Leu	Asn	Leu
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Tyr	Met	His	Gln	Val	Leu	Ile	Arg	Arg	Thr	Gly	Ile	Pro	Ile	Ser	Met
	290					295					300				
Ser	Leu	Leu	Tyr	Leu	Thr	Ile	Ala	Arg	Gln	Leu	Gly	Val	Pro	Leu	Glu
305					310					315					320
Pro	Val	Asn	Phe	Pro	Ser	His	Phe	Leu	Leu	Arg	Trp	Cys	Gln	Gly	Ala
				325					330					335	
Glu	Gly	Ala	Thr	Leu	Asp	Ile	Phe	Asp	Tyr	Ile	Tyr	Ile	Asp	Ala	Phe
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Gly	Lys	Gly	Lys	Gln	Leu	Thr	Val	Lys	Glu	Cys	Glu	Tyr	Leu	Ile	Gly
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Gln	His	Val	Thr	Ala	Ala	Leu	Tyr	Gly	Val	Val	Asn	Val	Lys	Lys	Val
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Leu	Gln	Arg	Met	Val	Gly	Asn	Leu	Leu	Ser	Leu	Gly	Lys	Arg	Glu	Gly
385					390					395					400
Ile	Asp	Gln	Ser	Tyr	Gln	Leu	Leu	Arg	Asp	Ser	Leu	Asp	Leu	Tyr	Leu
				405					410					415	
Ala	Met	Tyr	Pro	Asp	Gln	Val	Gln	Leu	Leu	Leu	Leu	Gln	Ala	Arg	Leu
			420					425					430		
Tyr	Phe	His	Leu	Gly	Ile	Trp	Pro	Glu	Lys	Val	Leu	Asp	Ile	Leu	Gln
		435				440					445				
His	Ile	Gln	Thr	Leu	Asp	Pro	Gly	Gln	His	Gly	Ala	Val	Gly	Tyr	Leu
	450					455					460				
Val	Gln	His	Thr	Leu	Glu	His	Ile	Glu	Arg	Lys	Lys	Glu	Glu	Val	Gly
465					470					475					480
Val	Glu	Val	Lys	Leu	Arg	Ser	Asp	Glu	Lys	His	Arg	Asp	Val	Cys	Tyr
				485					490					495	
Ser	Ile	Gly	Leu	Ile	Met	Lys	His	Lys	Arg	Tyr	Gly	Tyr	Asn	Cys	Val
			500					505					510		
Ile	Tyr	Gly	Trp	Asp	Pro	Thr	Cys	Met	Met	Gly	His	Glu	Trp	Ile	Arg
		515					520					525			

Asn Met Asn Val His Ser Leu Pro His Gly His His Gln Pro Phe Tyr
 530 535 540
 Asn Val Leu Val Glu Asp Gly Ser Cys Arg Tyr Ala Ala Gln Glu Asn
 545 550 555 560
 Leu Glu Tyr Asn Val Glu Pro Gln Glu Ile Ser His Pro Asp Val Gly
 565 570 575
 Arg Tyr Phe Ser Glu Phe Thr Gly Thr His Tyr Ile Pro Asn Ala Glu
 580 585 590
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 595 600 605
 Gln Asn Ile Tyr Ser Ala Lys Lys Glu Asn Ile Asp Glu
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<210> 29
 <211> 278
 <212> DNA
 <213> Homo sapiens

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 <222> all n positions
 <223> n=a, c, g or t

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<210> 30
 <211> 91
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> all Xaa positions
 <223> Xaa=unknown amino acid residue

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 20 25 30
 Ser Asn Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala
 35 40 45
 Lys Ala Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys
 50 55 60
 Val Arg Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile Ser Ala

65

70

75

80

Gly Leu Ala Glu Ala Gly His Leu Xaa Gly His
85 90

<210> 31

<211> 592

<212> DNA

<213> Homo sapiens

<400> 31

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<210> 32

<211> 197

<212> PRT

<213> Homo sapiens

<400> 32

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Pro Pro Gln Gln Gln Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro
35 40 45
Pro Pro Pro Leu Pro Gln Glu Arg Asn Asn Val Gly Glu Arg Asp Asp
50 55 60
Asp Val Pro Ala Asp Met Val Ala Glu Glu Ser Gly Pro Gly Ala Gln
65 70 75 80
Asn Ser Pro Tyr Gln Leu Arg Arg Lys Thr Leu Leu Pro Lys Arg Thr
85 90 95
Ala Cys Pro Thr Lys Asn Ser Met Glu Gly Ala Ser Thr Ser Thr Thr
100 105 110
Glu Asn Phe Gly His Arg Ala Lys Arg Ala Arg Val Ser Gly Lys Ser
115 120 125
Gln Asp Leu Ser Ala Ala Pro Ala Glu Gln Tyr Leu Gln Glu Lys Leu
130 135 140
Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln Asp
145 150 155 160
Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala Asn
165 170 175

Asp Pro Asn Leu Trp Lys Arg Leu Tyr Met Glu Val Phe Glu Tyr Thr
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Arg Pro Met Met His
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<211> 537
<212> DNA
<213> Homo sapiens

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<210> 34
<211> 178
<212> PRT
<213> Homo sapiens

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35 40 45
Trp Tyr Glu Leu Ile Leu Ser Leu Asp Ser Thr Arg Trp Arg Gln Leu
50 55 60
Cys Leu Gly Cys Thr Glu Cys Arg His Pro Asn Trp Pro Asn Gln Pro
65 70 75 80
Asp Val Glu Pro Glu Ser Trp Arg Glu Ala Phe Lys Gln His Tyr Leu
85 90 95
Ala Ser Lys Thr Trp Thr Lys Asn Ala Leu Asp Leu Glu Ser Ser Ile
100 105 110
Cys Phe Ser Leu Phe Arg Arg Arg Arg Glu Arg Arg Thr Leu Ser Val
115 120 125
Gly Pro Gly Arg Glu Phe Asp Ser Leu Gly Ser Ala Leu Ala Met Ala
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145 150 155 160
Gly Glu Ile Ile Leu Lys Val Pro Val Glu Ile Val Gly Gln Gly Lys

Leu Gly

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 <211> 751
 <212> DNA
 <213> Homo sapiens

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 gcatggcact gtctaatac tatcgttctg aagatttggt agacgtcgat acagctgccg 540
 gagattccag cagagacagg gactgaaata ctgtctccct ttaacttttg catacatact 600
 ggtttgagtc agtacatagc agtggaagct gcagagggtt gaaacaaaaa tgaagttttc 660
 taccaatgtc agacagtaga acgtgtgttt aaatatggca ttaagatgtg ttctgatggt 720
 tgtataaatg gcatgcatta ggtattttca g 751

<210> 36
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 36
 Glu Thr Glu Thr Ala Pro Leu Thr Leu Glu Ser Leu Pro Thr Asp Pro
 1 5 10 15
 Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg Asp Leu Ile Asn Cys
 20 25 30
 Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser Ser His Asp Pro Leu
 35 40 45
 Trp Arg Arg His Cys Lys Lys Tyr Trp Leu Ile Ser Glu Glu Glu Lys
 50 55 60
 Thr Gln Lys Asn Gln Cys Trp Lys Ser Leu Phe Ile Asp Thr Tyr Ser
 65 70 75 80
 Asp Val Gly Arg Tyr Ile Asp His Tyr Ala Ala Ile Lys Lys Ala Ser
 85 90 95
 Gly Met Ile Ser Arg Asn Ile Trp Ser Pro Gly Val Leu Gly Trp Val
 100 105 110
 Leu Ser Leu Lys Glu Gly Cys Ser Arg Gly Arg Pro Arg Cys Cys Gly
 115 120 125
 Ser Ala Asp Trp Ala Ala Ser Phe Leu Asp Asp Tyr Arg Cys Ser Tyr
 130 135 140
 Arg Ile His Asn Gly Gln Lys Leu Val Gly Ser Trp Gly Tyr Trp Glu
 145 150 155 160

Ala Trp His Cys Leu Ile Thr Ile Val Leu Lys Ile Cys Thr Ser Ile
165 170 175

Gln Leu Pro Glu Ile Pro Ala Glu Thr Gly Thr Glu Ile Leu Ser Pro
180 185 190

Phe Asn Phe Cys Ile His Thr Gly Leu Ser Gln Tyr Ile Ala Val Glu
195 200 205

Ala Ala Glu Gly Asn Lys Asn Glu Val Phe Tyr Gln Cys Gln Thr Val
210 215 220

Glu Arg Val Phe Lys Tyr Gly Ile Lys Met Cys Ser Asp Gly Cys Ile
225 230 235 240

Asn Gly Met His Val Phe Ser
245

<210> 37
<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> all n positions
<223> n=a, c, g or t

<400> 37
ggctccggtt tccggggccgg cgggtggccg ctcaccatgc ccggnaagca ccagcatttc 60
caggaacctg aggtcggtcg ctgcgggaaa tacttctgt ttgggttcaa cattgtcttc 120
tgggtgctgg gagccctgtt cctggctatc ggcctctggg cctgggggtga gaagggcggt 180
ctctcgaaca tctcagcgct gacagatctg ggaggccttg acccgtgtg gcttgtttgt 240
ggtagtgtga ggcgtcatgt cgggtgctggg ctttgctggg ctgcaattgg ggccctccgg 300
gagaacacct tcctgctcaa gtttttctnc gngttcctcg gtctcatctt cttcctggag 360
ctggcaac 368

<210> 38
<211> 122
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> all Xaa positions
<223> Xaa=unknown amino acid residue

<400> 38
Gly Ser Gly Phe Arg Ala Gly Gly Trp Pro Leu Thr Met Pro Gly Lys
1 5 10 15

His Gln His Phe Gln Glu Pro Glu Val Gly Cys Cys Gly Lys Tyr Phe
20 25 30

Leu Phe Gly Phe Asn Ile Val Phe Trp Val Leu Gly Ala Leu Phe Leu
35 40 45

Ala Ile Gly Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile
50 55 60

Ser Ala Leu Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys
 65 70 75 80

Gly Ser Trp Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala Ala Ile
 85 90 95

Gly Ala Leu Arg Glu Asn Thr Phe Leu Leu Lys Phe Phe Xaa Xaa Phe
 100 105 110

Leu Gly Leu Ile Phe Phe Leu Glu Leu Ala
 115 120

<210> 39
 <211> 774
 <212> DNA
 <213> Homo sapiens

<400> 39
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 gccgcactgc cggccgcgca gctgggtgcag gcctgcccgc tgggtgtgcct gcgctggaag 120
 gagctggtgg acggcgcccc gctgtggctg ctcaagtgcc agcaggaggg gctgggtgcc 180
 gagggcgccg tggaggagga gcgcgaccac tggcagcagt tctacttcct gagcaagcgg 240
 cgcgcgaacc ttctgcgtaa cccgtgtggg gaagaggact tggaaggctg gtgtgacgtg 300
 gagcatggtg gggacggctg gaggggtggag gagctgcctg gagacagtgg ggtggagttc 360
 acccacgatg agagcgtcaa gaagtacttc gcctcctcct ttgagtgggtg tcgcaaagca 420
 caggtcattg acctgcaggc tgagggctac tgggaggagc tgctggacac gactcagccg 480
 gccatcgtgg tgaaggactg gtactcgggc cgcagcgacg ctggttgccct ctacgagctc 540
 accgttaagc tactgtccga gcacgagaac gtgctggctg agttcagcag cgggcagggtg 600
 gcagtgcgcc aagacagtga cggcgggggc tggatggaga tctccacac cttcaccgac 660
 tacgggcccg gcgtccgctt cgtccgcttc gagcacgggg ggcaggggctc cgtctactgg 720
 aagggtggtg tcggggcccc ggtgaccaac agcagcgtgt gggtagaacc ctga 774

<210> 40
 <211> 257
 <212> PRT
 <213> Homo sapiens

<400> 40
 Ala Ala Ala Ala Ala Ala Tyr Leu Asp Glu Leu Pro Glu Pro Leu Leu
 1 5 10 15

Leu Arg Val Leu Ala Ala Leu Pro Ala Ala Glu Leu Val Gln Ala Cys
 20 25 30

Arg Leu Val Cys Leu Arg Trp Lys Glu Leu Val Asp Gly Ala Pro Leu
 35 40 45

Trp Leu Leu Lys Cys Gln Gln Glu Gly Leu Val Pro Glu Gly Gly Val
 50 55 60

Glu Glu Glu Arg Asp His Trp Gln Gln Phe Tyr Phe Leu Ser Lys Arg
 65 70 75 80

Arg Arg Asn Leu Leu Arg Asn Pro Cys Gly Glu Glu Asp Leu Glu Gly
 85 90 95

Trp Cys Asp Val Glu His Gly Gly Asp Gly Trp Arg Val Glu Glu Leu
 100 105 110

Pro Gly Asp Ser Gly Val Glu Phe Thr His Asp Glu Ser Val Lys Lys
 115 120 125
 Tyr Phe Ala Ser Ser Phe Glu Trp Cys Arg Lys Ala Gln Val Ile Asp
 130 135 140
 Leu Gln Ala Glu Gly Tyr Trp Glu Glu Leu Leu Asp Thr Thr Gln Pro
 145 150 155 160
 Ala Ile Val Val Lys Asp Trp Tyr Ser Gly Arg Ser Asp Ala Gly Cys
 165 170 175
 Leu Tyr Glu Leu Thr Val Lys Leu Leu Ser Glu His Glu Asn Val Leu
 180 185 190
 Ala Glu Phe Ser Ser Gly Gln Val Ala Val Pro Gln Asp Ser Asp Gly
 195 200 205
 Gly Gly Trp Met Glu Ile Ser His Thr Phe Thr Asp Tyr Gly Pro Gly
 210 215 220
 Val Arg Phe Val Arg Phe Glu His Gly Gly Gln Gly Ser Val Tyr Trp
 225 230 235 240
 Lys Gly Trp Phe Gly Ala Arg Val Thr Asn Ser Ser Val Trp Val Glu
 245 250 255

Pro

<210> 41
 <211> 957
 <212> DNA
 <213> Homo sapiens

<400> 41
 atgggcgaga aggcgggtccc ttgctaagg aggaggcggg tgaagagaag ctgcccttct 60
 tgtggctcgg agcttgggggt tgaagagaag agggggaaaag gaaatccgat ttccatccag 120
 ttgttcccc cagagctggg ggagcatatc atctcattcc tcccagtcag agacctgtgt 180
 gccctcggcc agacctgccg ctacttccac gaagtgtgcg atggggaagg cgtgtggaga 240
 cgcattctgtc gcagactcag tccgcgcctc caagatcagg acacgaaggg cctgtatttc 300
 caggcatttg gaggcgcgcg ccgatgtctc agcaagagcg tggccccctt gctagcccac 360
 ggctaccgcc gcttcttgcc caccaaggat cagctcttca ttcttgacta cgtggggacc 420
 ctcttcttcc tcaaaaatgc cctggtctcc accctcggcc agatgcagtg gaagcgggcc 480
 tgctcgctatg ttgtgttggt tcgtggagcc aaggattttg cctcggaccc aaggtgtgac 540
 acagtttacc gtaaatacct ctacgtcttg gccactcggg agccgcagga agtgggtggg 600
 accaccagca gccgggcctg tgactgtggt gaggtctatc tgcagtctag tgggcagcgg 660
 gtcttcaaga tgacattcca ccactcaatg accttcaagc agatcgtgct ggttggtcag 720
 gagaccagc gggctctact gctcctcaca gaggaaggaa agatctactc ttggtagtgt 780
 aatgagaccc agcttgacca gccacgctcc tacacggttc agctggccct gaggaagggtg 840
 tcccactacc tgcctcacct gcgcgtggcc tgcattgact ccaaccagag cagcaccctc 900
 tacgtcacag atcctattct gtgctcttgg ctacaaccac cttggcctgg tggatga 957

<210> 42
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 42
 Met Gly Glu Lys Ala Val Pro Leu Leu Arg Arg Arg Arg Val Lys Arg

1	5	10	15
Ser Cys Pro	Ser Cys Gly	Ser Glu Leu Gly Val Glu Glu Lys Arg Gly	
	20	25	30
Lys Gly Asn Pro Ile Ser Ile Gln Leu Phe Pro Pro Glu Leu Val Glu			
	35	40	45
His Ile Ile Ser Phe Leu Pro Val Arg Asp Leu Val Ala Leu Gly Gln			
	50	55	60
Thr Cys Arg Tyr Phe His Glu Val Cys Asp Gly Glu Gly Val Trp Arg			
	65	70	75
Arg Ile Cys Arg Arg Leu Ser Pro Arg Leu Gln Asp Gln Asp Thr Lys			
	85	90	95
Gly Leu Tyr Phe Gln Ala Phe Gly Gly Arg Arg Arg Cys Leu Ser Lys			
	100	105	110
Ser Val Ala Pro Leu Leu Ala His Gly Tyr Arg Arg Phe Leu Pro Thr			
	115	120	125
Lys Asp His Val Phe Ile Leu Asp Tyr Val Gly Thr Leu Phe Phe Leu			
	130	135	140
Lys Asn Ala Leu Val Ser Thr Leu Gly Gln Met Gln Trp Lys Arg Ala			
	145	150	155
Cys Arg Tyr Val Val Leu Cys Arg Gly Ala Lys Asp Phe Ala Ser Asp			
	165	170	175
Pro Arg Cys Asp Thr Val Tyr Arg Lys Tyr Leu Tyr Val Leu Ala Thr			
	180	185	190
Arg Glu Pro Gln Glu Val Val Gly Thr Thr Ser Ser Arg Ala Cys Asp			
	195	200	205
Cys Val Glu Val Tyr Leu Gln Ser Ser Gly Gln Arg Val Phe Lys Met			
	210	215	220
Thr Phe His His Ser Met Thr Phe Lys Gln Ile Val Leu Val Gly Gln			
	225	230	235
Glu Thr Gln Arg Ala Leu Leu Leu Leu Thr Glu Glu Gly Lys Ile Tyr			
	245	250	255
Ser Leu Val Val Asn Glu Thr Gln Leu Asp Gln Pro Arg Ser Tyr Thr			
	260	265	270
Val Gln Leu Ala Leu Arg Lys Val Ser His Tyr Leu Pro His Leu Arg			
	275	280	285
Val Ala Cys Met Thr Ser Asn Gln Ser Ser Thr Leu Tyr Val Thr Asp			
	290	295	300
Pro Ile Leu Cys Ser Trp Leu Gln Pro Pro Trp Pro Gly Gly			
	305	310	315

<210> 43

<211> 1590
 <212> DNA
 <213> Homo sapiens

<400> 43
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 aagaggaagc agggcggaag ggaagcccgg gccgcagacg gcgaaggagg cagcggggccg 120
 ggggctgagg cgggagcgag gacacgcccga agagaggaag cagagggagg cggaagcgtg 180
 gaggaagggg cgagaggcat catcaaagga gatgagggga gcgtaggggc cgggaaagag 240
 gcacaaggaa gaaagtatgg gaaggaggaa tggaggggtca gggctaggcg gcgggagggc 300
 gccaggccgg gaagagtaca aggacaagga ggtcagggtt gggcctacat cccggggaca 360
 ggggcggcca tggcggcggc agccaggag gagggaggagg aggcggctcg ggagtcagcc 420
 gcctgcccgg ctgcccgggc agcgcctctgg cgcctggccc aagtgtctgt gctgcacatg 480
 tgctcctacc tcgacatgcg ggccctcggc aggtgtaccg ctggctgtgg 540
 cacttcacca actgcgacct gctccggcgc cagatagcct gggcctcgct caactccggc 600
 ttcacgcggc tcggcaccaa cctgatgacc agtgtcccag tgaagggtgtc tcagaactgg 660
 atagtggggg gctgccgaga ggggattctg ctgaagtggg gatgcagtca gatgccctgg 720
 atgcagctag aggatgatgc tttgtacata tcccaggcta atttcatcct ggcctaccag 780
 ttccgtccag atgggtgccag cttgaaccgt cagcctctgg gactctctgc tgggcatgat 840
 gaggacgttt gccactttgt gctggccacc tcgcatattg tcagtgcagg aggagatggg 900
 aagattggcc ttggtaagat tcacagcacc ttgcgtgccga agtactgggc tcatgaacag 960
 gaggtgaact gtgtggattg caaagggggc atcatatcat ttggctccag ggacaggacg 1020
 gccaaaggtgt ggccttttgg ctcaggccag ctggggcagt gtttatacac catccagact 1080
 gaagacaaa tctggtctgt tgctatcagg ccattactca gctcttttgt gacagggacg 1140
 gcttggtgtg ggcacttctc acccctgaaa atctgggacc tcaacagtgg gcagctgatg 1200
 acacacttgg acagagactt tcccccaagg gctgggggtgc tggatgtcat atatgagtc 1260
 ccttttcgcac tgctctcctg tggctatgac acctatgttc gctactggga ctgccgcacc 1320
 agtggtccgga aatgtgtcat ggagtgggag gagccccaca acagcaccct gtactgctg 1380
 cagacagatg gcaaccactt gcttgccaca ggttcctcct tctatagcgt tgtacggctg 1440
 tgggaccggc accaaagggc ctgcccgcac accttcccgc tgacgtcgac ccgctcggc 1500
 agccctgtgt actgcctgca tctcaccacc aagcatctct atgctgcgct gtcttacaac 1560
 ctccacgtcc tggatattca aaaccgtga 1590

<210> 44
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 44
 Arg Gly Gly Ser Glu Gly Arg Gly Arg Gly Arg Glu Lys Arg Ala Arg
 1 5 10 15
 Gly Ala Arg Arg Lys Arg Lys Gln Gly Gly Arg Glu Ala Arg Ala Ala
 20 25 30
 Asp Gly Glu Gly Gly Ser Gly Pro Gly Ala Glu Ala Gly Ala Arg Thr
 35 40 45
 Arg Pro Arg Glu Glu Ala Glu Gly Gly Gly Ser Val Glu Glu Gly Ala
 50 55 60
 Arg Gly Ile Ile Lys Gly Asp Glu Gly Ser Val Gly Ala Gly Lys Glu
 65 70 75 80
 Ala Gln Gly Arg Lys Tyr Gly Lys Glu Glu Trp Arg Val Arg Ala Arg
 85 90 95
 Arg Arg Glu Gly Ala Arg Pro Gly Arg Val Gln Gly Gln Gly Gly Gln
 100 105 110
 Val Trp Ala Tyr Ile Pro Gly Thr Gly Ala Ala Met Ala Ala Ala Ala

115					120					125						
Arg	Glu	Glu	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Ser	Ala	Ala	Cys	Pro	Ala	
130					135					140						
Ala	Gly	Pro	Ala	Leu	Trp	Arg	Leu	Pro	Glu	Val	Leu	Leu	Leu	His	Met	
145					150					155					160	
Cys	Ser	Tyr	Leu	Asp	Met	Arg	Ala	Leu	Gly	Arg	Leu	Ala	Gln	Val	Tyr	
165					170					175						
Arg	Trp	Leu	Trp	His	Phe	Thr	Asn	Cys	Asp	Leu	Leu	Arg	Arg	Gln	Ile	
180					185					190						
Ala	Trp	Ala	Ser	Leu	Asn	Ser	Gly	Phe	Thr	Arg	Leu	Gly	Thr	Asn	Leu	
195					200					205						
Met	Thr	Ser	Val	Pro	Val	Lys	Val	Ser	Gln	Asn	Trp	Ile	Val	Gly	Cys	
210					215					220						
Cys	Arg	Glu	Gly	Ile	Leu	Leu	Lys	Trp	Arg	Cys	Ser	Gln	Met	Pro	Trp	
225					230					235					240	
Met	Gln	Leu	Glu	Asp	Asp	Ala	Leu	Tyr	Ile	Ser	Gln	Ala	Asn	Phe	Ile	
245					250					255						
Leu	Ala	Tyr	Gln	Phe	Arg	Pro	Asp	Gly	Ala	Ser	Leu	Asn	Arg	Gln	Pro	
260					265					270						
Leu	Gly	Val	Ser	Ala	Gly	His	Asp	Glu	Asp	Val	Cys	His	Phe	Val	Leu	
275					280					285						
Ala	Thr	Ser	His	Ile	Val	Ser	Ala	Gly	Gly	Asp	Gly	Lys	Ile	Gly	Leu	
290					295					300						
Gly	Lys	Ile	His	Ser	Thr	Phe	Ala	Ala	Lys	Tyr	Trp	Ala	His	Glu	Gln	
305					310					315					320	
Glu	Val	Asn	Cys	Val	Asp	Cys	Lys	Gly	Gly	Ile	Ile	Ser	Phe	Gly	Ser	
325					330					335						
Arg	Asp	Arg	Thr	Ala	Lys	Val	Trp	Pro	Leu	Ala	Ser	Gly	Gln	Leu	Gly	
340					345					350						
Gln	Cys	Leu	Tyr	Thr	Ile	Gln	Thr	Glu	Asp	Gln	Ile	Trp	Ser	Val	Ala	
355					360					365						
Ile	Arg	Pro	Leu	Leu	Ser	Ser	Phe	Val	Thr	Gly	Thr	Ala	Cys	Cys	Gly	
370					375					380						
His	Phe	Ser	Pro	Leu	Lys	Ile	Trp	Asp	Leu	Asn	Ser	Gly	Gln	Leu	Met	
385					390					395					400	
Thr	His	Leu	Asp	Arg	Asp	Phe	Pro	Pro	Arg	Ala	Gly	Val	Leu	Asp	Val	
405					410					415						
Ile	Tyr	Glu	Ser	Pro	Phe	Ala	Leu	Leu	Ser	Cys	Gly	Tyr	Asp	Thr	Tyr	
420					425					430						
Val	Arg	Tyr	Trp	Asp	Cys	Arg	Thr	Ser	Val	Arg	Lys	Cys	Val	Met	Glu	
435					440					445						

Trp Glu Glu Pro His Asn Ser Thr Leu Tyr Cys Leu Gln Thr Asp Gly
 450 455 460
 Asn His Leu Leu Ala Thr Gly Ser Ser Phe Tyr Ser Val Val Arg Leu
 465 470 475 480
 Trp Asp Arg His Gln Arg Ala Cys Pro His Thr Phe Pro Leu Thr Ser
 485 490 495
 Thr Arg Leu Gly Ser Pro Val Tyr Cys Leu His Leu Thr Thr Lys His
 500 505 510
 Leu Tyr Ala Ala Leu Ser Tyr Asn Leu His Val Leu Asp Ile Gln Asn
 515 520 525

Pro

<210> 45
 <211> 1214
 <212> DNA
 <213> Homo sapiens

<400> 45
 gcattgctat aatttttacta tactctcatc taaatctaaa atcagtcttc aaaataaaaa 60
 caaattgtcc ttgcccacaa atttttttaa tcgcacaatt aattgacatt aactgccaat 120
 tctttttggc taattgacta attttaactt ctgtgttgct tttccagagg catggctatt 180
 gcaccttggg agaagccttt aatcgggttag acttctcaag tgcaattcaa gatatccgaa 240
 cgttcaatta tgtggtcaaa ctgttgagc taattgcaaa atcccagtta acttcattga 300
 gtggcgtggc acagaagaat tacttcaaca ttttgataa aatcgttcaa aagggttcttg 360
 atgaccacca caatcctcgc ttaatcaaag atcttctgca agacctaaag tctaccctct 420
 gcattcttat tagaggagta gggaagtctg tattagtggg aaacatcaat atttggattt 480
 gccgattaga aactattctc gcctggcaac aacagctaca ggatcttcag atgactaagc 540
 aagtgaacaa tggcctcacc ctgagtacc ttctctgca catgctgaac aacatcctat 600
 accggttctc agacggatgg gacatcatca ccttaggcca ggtgacccc acgttgata 660
 tgcttagtga agacagacag ctgtggaaga agctttgtca gtaccatttt gctgaaaagc 720
 agttttgtag acatttgatc ctttcagaaa aaggtcatat tgaatggaag ttgatgtact 780
 ttgacttca gaaacattac ccagcgaagg agcagtacgg agacacactg catttctgtc 840
 ggcactgcag cattctcttt tggaaggact caggacaccc ctgcacggcg gccgaccctg 900
 acagctgctt cacgcctgtg tctccgcagc acttcatcga cctcttcaag ttttaagggc 960
 tgcccctgcc atccctattg gagattgtga atcctgctgt ctgtgcaggg ctcatagtga 1020
 gtgttctgtg aggtgggtgg agactcctcg gaagcccctg cttccagaaa gcctgggaag 1080
 aactgccctt ctgcaaaggg gggactgcat ggttgcatth tcatcactga aagtcagagg 1140
 ccaaggaaat catttctact tctttaaaaa ctcttctaa gcatattaaa atgtgaaatt 1200
 ttgcgtactc tctc 1214

<210> 46
 <211> 272
 <212> PRT
 <213> Homo sapiens

<400> 46
 Leu Ile Leu Thr Ser Val Leu Leu Phe Gln Arg His Gly Tyr Cys Thr
 1 5 10 15
 Leu Gly Glu Ala Phe Asn Arg Leu Asp Phe Ser Ser Ala Ile Gln Asp
 20 25 30
 Ile Arg Thr Phe Asn Tyr Val Val Lys Leu Leu Gln Leu Ile Ala Lys

35

40

45

Ser Gln Leu Thr Ser Leu Ser Gly Val Ala Gln Lys Asn Tyr Phe Asn
 50 55 60
 Ile Leu Asp Lys Ile Val Gln Lys Val Leu Asp Asp His His Asn Pro
 65 70 75 80
 Arg Leu Ile Lys Asp Leu Leu Gln Asp Leu Ser Ser Thr Leu Cys Ile
 85 90 95
 Leu Ile Arg Gly Val Gly Lys Ser Val Leu Val Gly Asn Ile Asn Ile
 100 105 110
 Trp Ile Cys Arg Leu Glu Thr Ile Leu Ala Trp Gln Gln Gln Leu Gln
 115 120 125
 Asp Leu Gln Met Thr Lys Gln Val Asn Asn Gly Leu Thr Leu Ser Asp
 130 135 140
 Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly
 145 150 155 160
 Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu
 165 170 175
 Ser Glu Asp Arg Gln Leu Trp Lys Lys Leu Cys Gln Tyr His Phe Ala
 180 185 190
 Glu Lys Gln Phe Cys Arg His Leu Ile Leu Ser Glu Lys Gly His Ile
 195 200 205
 Glu Trp Lys Leu Met Tyr Phe Ala Leu Gln Lys His Tyr Pro Ala Lys
 210 215 220
 Glu Gln Tyr Gly Asp Thr Leu His Phe Cys Arg His Cys Ser Ile Leu
 225 230 235 240
 Phe Trp Lys Asp Ser Gly His Pro Cys Thr Ala Ala Asp Pro Asp Ser
 245 250 255
 Cys Phe Thr Pro Val Ser Pro Gln His Phe Ile Asp Leu Phe Lys Phe
 260 265 270

<210> 47

<211> 4059

<212> DNA

<213> Homo sapiens

<400> 47

agtacggcag tgagggcaaa ggcagctcga gcatctcatc tgacgtgagt tcaagtacag 60
 atcacacgcc cactaaagcc cagaagaatg tggctaccag cgaagactcc gacctgagca 120
 tgcgcacact gagcacgcc agcccagccc tgatatgtcc accgaatctc ccaggatttc 180
 agaatggaag gggctcgtcc acctcctcgt cctccatcac cggggagacg gtggccatgg 240
 tgcactcccc gccccgacc cgctcacac acccgctcat ccggctcgcc tccagacccc 300
 agaaggagca ggccagcata gaccggctcc cggaccactc catggtgcag atcttctcct 360
 tcctgcccac caaccagctg tgccgctgcg cgcgagtgtg ccgccgctgg tacaacctgg 420
 cctgggaccc gcggctctgg aggactatcc gcctgacggg cgagaccatc aacgtggacc 480

gcgcccctcaa	ggtgctgacc	cgcagactct	gccaggacac	ccccaacgtg	tgtctcatgc	540
tggaaaccgt	aactgtcagt	ggctgcaggc	ggctcacaga	ccgaggggctg	tacaccatcg	600
cccagtgctg	ccccgaactg	aggcgactgg	aagtctcagg	ctgttacaat	atctccaacg	660
aggccgtctt	tgatgtggtg	tccctctgcc	ctaatctgga	gcacctggat	gtgtcaggat	720
gctccaaaagt	gacctgcatc	agcttgaccc	gggaggcctc	cattaaaactg	tcacccttgc	780
atggcaaaaca	gattttccatc	cgctacctgg	acatgacgga	ctgcttcgtg	ctggaggagc	840
aaggcctgca	caccatcgcg	gcgcactgca	cgcagctcac	ccacctctac	ctgcgccgct	900
gcgtccgcct	gaccgacgaa	ggcctgcgct	acctggtgat	ctactgcgcc	tccatcaagg	960
agctgagcgt	cagcgactgc	cgcttcgtca	gcgacttcgg	cctgcgggag	atcgccaagc	1020
tggagtcccg	cctgcggtac	ctgagcatcg	cgactgcgg	ccgggtcacc	gacgtgggca	1080
tccgctacgt	ggccaagtac	tgcagcaagc	tgcgctacct	caacgcgagg	ggctgcgagg	1140
gcatcacgga	ccacggtgtg	gagtacctcg	ccaagaactg	cacaaaactc	aaatccctgg	1200
atatcggcaa	atgccctttg	gtatccgaca	ggggcctgga	gtgcctggcc	ctgaactgct	1260
tcaacctcaa	gcgggtcagc	ctcaagtcct	gcgagagcat	caccggccag	ggcttgccaga	1320
tcgtggccgc	caactgcttt	gacctccaga	cgctgaatgt	ccaggactgc	gaggtctccg	1380
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<210> 48
 <211> 483
 <212> PRT
 <213> Homo sapiens

<400> 48

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Ser	Glu	Asp	Ser	Asp	Leu	Ser	Met	Arg	Thr	Leu	Ser	Thr	Pro	Ser	Pro	35	40	45	
Ala	Leu	Ile	Cys	Pro	Pro	Asn	Leu	Pro	Gly	Phe	Gln	Asn	Gly	Arg	Gly	50	55	60	
Ser	Ser	Thr	Ser	Ser	Ser	Ser	Ile	Thr	Gly	Glu	Thr	Val	Ala	Met	Val	65	70	75	80
His	Ser	Pro	Pro	Pro	Thr	Arg	Leu	Thr	His	Pro	Leu	Ile	Arg	Leu	Ala	85	90	95	
Ser	Arg	Pro	Gln	Lys	Glu	Gln	Ala	Ser	Ile	Asp	Arg	Leu	Pro	Asp	His	100	105	110	
Ser	Met	Val	Gln	Ile	Phe	Ser	Phe	Leu	Pro	Thr	Asn	Gln	Leu	Cys	Arg	115	120	125	
Cys	Ala	Arg	Val	Cys	Arg	Arg	Trp	Tyr	Asn	Leu	Ala	Trp	Asp	Pro	Arg	130	135	140	
Leu	Trp	Arg	Thr	Ile	Arg	Leu	Thr	Gly	Glu	Thr	Ile	Asn	Val	Asp	Arg	145	150	155	160
Ala	Leu	Lys	Val	Leu	Thr	Arg	Arg	Leu	Cys	Gln	Asp	Thr	Pro	Asn	Val	165	170	175	
Cys	Leu	Met	Leu	Glu	Thr	Val	Thr	Val	Ser	Gly	Cys	Arg	Arg	Leu	Thr	180	185	190	
Asp	Arg	Gly	Leu	Tyr	Thr	Ile	Ala	Gln	Cys	Cys	Pro	Glu	Leu	Arg	Arg	195	200	205	
Leu	Glu	Val	Ser	Gly	Cys	Tyr	Asn	Ile	Ser	Asn	Glu	Ala	Val	Phe	Asp	210	215	220	
Val	Val	Ser	Leu	Cys	Pro	Asn	Leu	Glu	His	Leu	Asp	Val	Ser	Gly	Cys	225	230	235	240
Ser	Lys	Val	Thr	Cys	Ile	Ser	Leu	Thr	Arg	Glu	Ala	Ser	Ile	Lys	Leu	245	250	255	
Ser	Pro	Leu	His	Gly	Lys	Gln	Ile	Ser	Ile	Arg	Tyr	Leu	Asp	Met	Thr	260	265	270	
Asp	Cys	Phe	Val	Leu	Glu	Asp	Glu	Gly	Leu	His	Thr	Ile	Ala	Ala	His	275	280	285	
Cys	Thr	Gln	Leu	Thr	His	Leu	Tyr	Leu	Arg	Arg	Cys	Val	Arg	Leu	Thr				

290	295	300
Asp Glu Gly Leu Arg Tyr Leu Val Ile Tyr Cys Ala Ser Ile Lys Glu 305 310 315 320		
Leu Ser Val Ser Asp Cys Arg Phe Val Ser Asp Phe Gly Leu Arg Glu 325 330 335		
Ile Ala Lys Leu Glu Ser Arg Leu Arg Tyr Leu Ser Ile Ala His Cys 340 345 350		
Gly Arg Val Thr Asp Val Gly Ile Arg Tyr Val Ala Lys Tyr Cys Ser 355 360 365		
Lys Leu Arg Tyr Leu Asn Ala Arg Gly Cys Glu Gly Ile Thr Asp His 370 375 380		
Gly Val Glu Tyr Leu Ala Lys Asn Cys Thr Lys Leu Lys Ser Leu Asp 385 390 395 400		
Ile Gly Lys Cys Pro Leu Val Ser Asp Thr Gly Leu Glu Cys Leu Ala 405 410 415		
Leu Asn Cys Phe Asn Leu Lys Arg Leu Ser Leu Lys Ser Cys Glu Ser 420 425 430		
Ile Thr Gly Gln Gly Leu Gln Ile Val Ala Ala Asn Cys Phe Asp Leu 435 440 445		
Gln Thr Leu Asn Val Gln Asp Cys Glu Val Ser Val Glu Ala Leu Arg 450 455 460		
Phe Val Lys Arg His Cys Lys Arg Cys Val Ile Glu His Thr Asn Pro 465 470 475 480		
Ala Phe Phe		

<210> 49
 <211> 850
 <212> DNA
 <213> Homo sapiens

<400> 49
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 ggcggacggc cccatgccct tcctgggcag ggctgcgcgc gtgtgccgcc gctggcagga 180
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 ctgccacggg gtgactgtgt acgctctggt catgctagcc aaagcctgct gccagctcca 480
 tagcctggac ctacagcact ccatggtgga gtccacagct gtggtgagct tcttgaggga 540
 ggcagggtcc cgaatgcgca agttgtggct gacctacagc tccagacga cagccatcct 600
 gggcgcatgt ctgggcagct gctgccccca gctccaggtc ctggaggtga gcaccggcat 660
 caaccgtaat agcattcccc ttcagctgcc tgtcagggt ctgcagaaag gctgccctca 720
 gctccagggt ctgcggctgt tgaacctgat gtggctgccc aagcctccgg gacgaggggt 780
 ggctcccga ccaggcttcc ctgacctaga ggagctctgc ctggcgagct caacctgcaa 840
 ctttgtgagc 850

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens
 <400> 50
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 Gly Pro Asp Ala Gly Trp Gly Asp Arg Ile Pro Leu Glu Ile Leu Val
 20 25 30
 Gln Ile Phe Gly Leu Leu Val Ala Ala Asp Gly Pro Met Pro Phe Leu
 35 40 45
 Gly Arg Ala Ala Arg Val Cys Arg Arg Trp Gln Glu Ala Ala Ser Gln
 50 55 60
 Pro Ala Leu Trp His Thr Val Thr Leu Ser Ser Pro Leu Val Gly Arg
 65 70 75 80
 Pro Ala Lys Gly Gly Val Lys Ala Glu Lys Lys Leu Leu Ala Ser Leu
 85 90 95
 Glu Trp Leu Met Pro Asn Arg Phe Ser Gln Leu Gln Arg Leu Thr Leu
 100 105 110
 Ile His Trp Lys Ser Gln Val His Pro Val Leu Lys Leu Val Gly Glu
 115 120 125
 Cys Cys Pro Arg Leu Thr Phe Leu Lys Leu Ser Gly Cys His Gly Val
 130 135 140
 Thr Ala Asp Ala Leu Val Met Leu Ala Lys Ala Cys Cys Gln Leu His
 145 150 155 160
 Ser Leu Asp Leu Gln His Ser Met Val Glu Ser Thr Ala Val Val Ser
 165 170 175
 Phe Leu Glu Glu Ala Gly Ser Arg Met Arg Lys Leu Trp Leu Thr Tyr
 180 185 190
 Ser Ser Gln Thr Thr Ala Ile Leu Gly Ala Leu Leu Gly Ser Cys Cys
 195 200 205
 Pro Gln Leu Gln Val Leu Glu Val Ser Thr Gly Ile Asn Arg Asn Ser
 210 215 220
 Ile Pro Leu Gln Leu Pro Val Glu Ala Leu Gln Lys Gly Cys Pro Gln
 225 230 235 240
 Leu Gln Val Leu Arg Leu Leu Asn Leu Met Trp Leu Pro Lys Pro Pro
 245 250 255
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 Cys Leu Ala Ser Ser Thr Cys Asn Phe Val Ser
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<210> 51

<211> 1777
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> all n positions
 <223> n=a, c, g or t

<400> 51
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 agaagtgtca gaacactcca caggtataac ccattcttcc cctgaggtaa tgctgtcaat 180
 tttcagctat cttaatcctc aagagtattg tcgatgcagt caagtaagca tgaaatgggtc 240
 tcagctgaca aaaacgggat cgctttggaa acatctttac cctgttcatt gggccagagg 300
 tgactgggat agtgggtccc caactgaact tgatactgaa cctgatgatg aatgggtgaa 360
 aaataggaaa gatgaaagtc gtgcttttca tgagtgggat gaagatgctg acattgatga 420
 atctgaagag tctgcggagg aatcaattgc tatcagcatt gcacaaatgg aaaaacggtt 480
 actccatggc ttaattcata acgttctacc atatgttggg acttctgtaa aaaccttagt 540
 attagcatat agctctgcag tttccagcaa aatgggttagg cagatttttag agctttgtcc 600
 taacctggag catctggatc ttaccagac tgacatttca gattctgcat ttgacagttg 660
 gtcttggtt ggttgctgcc agagtcttcg gcattcttgat ctgtctgggt gtgagaaaat 720
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<210> 52
 <211> 590
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> all Xaa positions
 <223> Xaa=unknown amino acid residue

<400> 52
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 Asp Glu Lys Ser Asp Lys Glu Ala Glu Val Ser Glu His Ser Thr Gly
 35 40 45

Ile Thr His Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu
 50 55 60
 Asn Pro Gln Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser
 65 70 75 80
 Gln Leu Thr Lys Thr Gly Ser Leu Trp Lys His Leu Tyr Pro Val His
 85 90 95
 Trp Ala Arg Gly Asp Trp Tyr Ser Gly Pro Ala Thr Glu Leu Asp Thr
 100 105 110
 Glu Pro Asp Asp Glu Trp Val Lys Asn Arg Lys Asp Glu Ser Arg Ala
 115 120 125
 Phe His Glu Trp Asp Glu Asp Ala Asp Ile Asp Glu Ser Glu Glu Ser
 130 135 140
 Ala Glu Glu Ser Ile Ala Ile Ser Ile Ala Gln Met Glu Lys Arg Leu
 145 150 155 160
 Leu His Gly Leu Ile His Asn Val Leu Pro Tyr Val Gly Thr Ser Val
 165 170 175
 Lys Thr Leu Val Leu Ala Tyr Ser Ser Ala Val Ser Ser Lys Met Val
 180 185 190
 Arg Gln Ile Leu Glu Leu Cys Pro Asn Leu Glu His Leu Asp Leu Thr
 Gln Thr Asp Ile Ser Asp Ser Ala Phe Asp Ser Trp Ser Trp Leu Gly
 210 215 220
 Cys Cys Gln Ser Leu Arg His Leu Asp Leu Ser Gly Cys Glu Lys Ile
 225 230 235 240
 Thr Asp Val Ala Leu Glu Lys Ile Ser Arg Ala Leu Gly Ile Leu Thr
 245 250 255
 Ser His Gln Ser Gly Phe Leu Lys Thr Ser Thr Ser Lys Ile Thr Ser
 260 265 270
 Thr Ala Trp Lys Asn Lys Asp Ile Thr Met Gln Ser Thr Lys Gln Tyr
 275 280 285
 Ala Cys Leu His Asp Leu Thr Asn Lys Gly Ile Gly Glu Glu Ile Asp
 290 295 300
 Asn Glu His Pro Trp Thr Lys Pro Val Ser Ser Glu Asn Phe Thr Ser
 305 310 315 320
 Pro Tyr Val Trp Met Leu Asp Ala Glu Asp Leu Ala Asp Ile Glu Asp
 325 330 335
 Thr Val Glu Trp Arg His Arg Asn Val Glu Ser Leu Cys Val Met Glu
 340 345 350
 Thr Ala Ser Asn Phe Ser Cys Ser Thr Ser Gly Cys Phe Ser Lys Asp
 355 360 365
 Ile Val Gly Leu Arg Thr Ser Val Cys Trp Gln Gln His Cys Ala Ser
 370 375 380

Pro Ala Phe Ala Tyr Cys Gly His Ser Phe Cys Cys Thr Gly Thr Ala
 385 390 395 400
 Leu Arg Thr Met Ser Ser Leu Pro Glu Ser Ser Ala Met Cys Arg Lys
 405 410 415
 Ala Ala Arg Thr Arg Leu Pro Arg Gly Lys Asp Leu Ile Tyr Phe Gly
 420 425 430
 Ser Glu Lys Ser Asp Gln Glu Thr Gly Arg Val Leu Leu Phe Leu Ser
 435 440 445
 Leu Ser Gly Cys Tyr Gln Ile Thr Asp His Gly Leu Arg Val Leu Thr
 450 455 460
 Leu Gly Gly Gly Leu Pro Tyr Leu Glu His Leu Asn Leu Ser Gly Cys
 465 470 475 480
 Leu Thr Ile Thr Gly Ala Gly Leu Gln Asp Leu Val Ser Ala Cys Pro
 485 490 495
 Ser Leu Asn Asp Glu Tyr Phe Tyr Tyr Cys Asp Asn Ile Asn Gly Pro
 500 505 510
 His Ala Asp Thr Ala Ser Gly Cys Gln Asn Leu Gln Cys Gly Phe Arg
 515 520 525
 Ala Cys Cys Arg Ser Gly Glu Pro Leu Thr Ser Asp Leu Cys Leu Leu
 530 535 540
 His Leu Ala Glu Gln Ala Phe Phe His Ala Leu Tyr Ser His Ile Ser
 545 550 555 560
 Cys Val Asn His Pro Phe Leu Ser Val Thr Cys Phe Gly Pro Ile Xaa
 565 570 575
 Tyr Asn Phe Arg Asn Leu Asn Tyr Gln Xaa Ile Val Met Leu
 580 585 590

<210> 53
 <211> 1681
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> all n positions
 <223> n=a, c, g or t

<400> 53
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 gagggcaaaa ggagcactag ctaggtcaga gccatgtttc aggtcacaat gtgatgtcag 180
 atgttgctta taaatccttt cttgtcttcg ccattcttaa atcttgatag gtgcctgttg 240
 ggaaactgta aatgcctttc ccaatggaga atcaacagat tgggtgatgg tggagtcggt 300
 caggaagact caggctcttc agaggaaagg atgcctcatc accccttngg cccaggcagc 360
 tgctgtcaga gaatgacaca gcacctgcac agtcgctgtc cacttcctgc cactgctgtc 420
 ggtgggggtga cgggagcaaa gtaggcgtgg actttgacat gagggagctg agcccgcatc 480
 cgcttgatgc ctgcacgggt aacctgctgg cagtcgtaca gtcgaggcg ctccaggcct 540
 cggcagttct ctagggtgtc cagggccaca tcagtgtatga ggaggcagtt gtccaactcc 600

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tggatgagtg tgctgtcggg tatcaggatg cawtcttcaa gatccatctt ctccaattcg 780
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ttgctgcaac ccgaaaggca gagagcctgt agccggtgac agcccctgca tatctgcacc 960
acaccttcat ccgtgatacg tgagcaggac tgcaagttga ggctcacaag ctcatggcag 1020
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gctaagatgt tccaagcctt ggaaatctgt gcacatcggc acaaagttac tatatccaag 1560
aaggaaaata ttcttaacag aagttctttg ggtaactttt tgtaataaag gccttcatca 1620
ttgtttgaga aaaccatggc cgaagagccg cgagcgagcc cacagcccga agtcacacgg 1680
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<210> 54

<211> 437

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> all Xaa positions

<223> Xaa=unknown amino acid residue

<400> 54

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Arg Val Thr Ser Gly Cys Gly Leu Ala Arg Gly Ser Ser Ala Met Val
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Phe Ser Asn Asn Asp Glu Gly Leu Ile Asn Lys Lys Leu Pro Lys Glu
      20              25              30

Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val Thr Leu Cys Arg
      35              40              45

Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala Leu Asp Gly Ser
      50              55              60

Asn Trp Gln Arg Ile Asp Leu Phe Asn Phe Gln Ile Asp Val Glu Gly
      65              70              75              80

Arg Val Val Glu Asn Ile Ser Lys Arg Cys Val Gly Phe Leu Arg Lys
      85              90              95

Leu Ser Leu Arg Gly Cys Ile Gly Val Gly Asp Ser Ser Leu Lys Thr
      100             105             110

Phe Ala Gln Asn Cys Arg Asn Ile Glu His Leu Asn Leu Asn Gly Cys
      115             120             125

Thr Lys Ile Thr Asp Ser Thr Cys Tyr Ser Leu Ser Arg Phe Cys Ser
      130             135             140

Lys Leu Lys His Leu Xaa Leu Thr Ser Cys Val Ser Ile Thr Asn Ser
      145             150             155             160

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Ser Leu Lys Gly Ile Ser Glu Gly Cys Arg Asn Leu Glu Tyr Leu Asn
 165 170 175
 Leu Ser Trp Cys Asp Gln Ile Thr Lys Asp Gly Ile Glu Ala Leu Val
 180 185 190
 Arg Gly Cys Arg Gly Leu Lys Ala Leu Leu Leu Arg Gly Cys Thr Gln
 195 200 205
 Leu Glu Asp Glu Ala Leu Lys His Ile Gln Asn Tyr Cys His Glu Leu
 210 215 220
 Val Ser Leu Asn Leu Gln Ser Cys Ser Arg Ile Thr Asp Glu Gly Val
 225 230 235 240
 Val Gln Ile Cys Arg Gly Cys His Arg Leu Gln Ala Leu Cys Leu Ser
 245 250 255
 Gly Cys Ser Asn Leu Thr Asp Ala Ser Leu Thr Ala Leu Gly Leu Asn
 260 265 270
 Cys Pro Arg Leu Gln Ile Leu Glu Ala Ala Arg Cys Ser His Leu Thr
 275 280 285
 Asp Ala Gly Phe Thr Leu Leu Ala Arg Asn Cys His Glu Leu Glu Lys
 290 295 300
 Met Asp Leu Glu Xaa Cys Ile Leu Ile Thr Asp Ser Thr Leu Ile Gln
 305 310 315 320
 Leu Ser Ile His Cys Pro Lys Leu Gln Ala Leu Ser Leu Ser His Cys
 325 330 335
 Glu Leu Ile Xaa Asp Asp Gly Ile Leu His Leu Ser Asn Ser Thr Cys
 340 345 350
 Gly His Glu Arg Leu Arg Val Leu Glu Leu Asp Asn Cys Leu Leu Ile
 355 360 365
 Thr Asp Val Ala Leu Xaa His Leu Glu Asn Cys Arg Gly Leu Glu Arg
 370 375 380
 Leu Glu Leu Tyr Asp Cys Gln Gln Val Thr Arg Ala Gly Ile Lys Arg
 385 390 395 400
 Met Arg Ala Gln Leu Pro His Val Lys Val His Ala Tyr Phe Ala Pro
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 420 425 430
 Cys Cys Val Ile Leu
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<210> 55
 <211> 1866
 <212> DNA
 <213> Homo sapiens
 <400> 55

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<210> 56

<211> 621

<212> PRT

<213> Homo sapiens

<400> 56

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Ile Cys Leu Arg Arg Arg Ala Arg Thr Ala Thr Arg Gly Glu Met Met
      20                      25                      30

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Asn Thr His Arg Ala Ile Glu Ser Asn Ser Gln Thr Ser Pro Leu Asn
  35                      40                      45

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Ala Glu Val Val Gln Tyr Ala Lys Glu Val Val Asp Phe Ser Ser His
  50                      55                      60

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Tyr Gly Ser Glu Asn Ser Met Ser Tyr Thr Met Trp Asn Leu Ala Gly
  65                      70                      75                      80

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```

Val Pro Asn Val Phe Pro Ser Ser Gly Asp Phe Thr Gln Thr Ala Val
      85                      90                      95

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Phe Arg Thr Tyr Gly Thr Trp Trp Asp Gln Cys Pro Ser Ala Ser Leu
  100                      105                      110

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Pro Phe Lys Arg Thr Pro Pro Asn Phe Gln Ser Gln Asp Tyr Val Glu

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115					120					125					
Leu	Thr	Phe	Glu	Gln	Gln	Val	Tyr	Pro	Thr	Ala	Val	His	Val	Leu	Glu
130						135					140				
Thr	Tyr	His	Pro	Gly	Ala	Val	Ile	Arg	Ile	Leu	Ala	Cys	Ser	Ala	Asn
145					150					155					160
Pro	Tyr	Ser	Pro	Asn	Pro	Pro	Ala	Glu	Val	Arg	Trp	Glu	Ile	Leu	Trp
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Ser	Glu	Arg	Pro	Thr	Lys	Val	Asn	Ala	Ser	Gln	Ala	Arg	Gln	Phe	Lys
			180					185					190		
Pro	Cys	Ile	Lys	Gln	Ile	Asn	Phe	Pro	Thr	Asn	Leu	Ile	Arg	Leu	Glu
	195						200					205			
Val	Asn	Ser	Ser	Leu	Leu	Glu	Tyr	Tyr	Thr	Glu	Leu	Asp	Ala	Val	Val
	210					215						220			
Leu	His	Gly	Val	Lys	Asp	Lys	Pro	Val	Leu	Ser	Leu	Lys	Thr	Ser	Leu
225					230					235					240
Ile	Asp	Met	Asn	Asp	Ile	Glu	Asp	Asp	Ala	Tyr	Ala	Glu	Lys	Asp	Gly
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Cys	Gly	Met	Asp	Ser	Leu	Asn	Lys	Lys	Phe	Ser	Ser	Ala	Val	Leu	Gly
			260					265					270		
Glu	Gly	Pro	Asn	Asn	Gly	Tyr	Phe	Asp	Lys	Leu	Pro	Tyr	Glu	Leu	Ile
		275					280						285		
Gln	Leu	Ile	Leu	Asn	His	Leu	Thr	Leu	Pro	Asp	Leu	Cys	Arg	Leu	Ala
	290					295					300				
Gln	Thr	Cys	Lys	Leu	Leu	Ser	Gln	His	Cys	Cys	Asp	Pro	Leu	Gln	Tyr
305					310					315					320
Ile	His	Leu	Asn	Leu	Gln	Pro	Tyr	Trp	Ala	Lys	Leu	Asp	Asp	Thr	Ser
				325					330					335	
Leu	Glu	Phe	Leu	Gln	Ser	Arg	Cys	Thr	Leu	Val	Gln	Trp	Leu	Asn	Leu
			340					345					350		
Ser	Trp	Thr	Gly	Asn	Arg	Gly	Phe	Ile	Ser	Val	Ala	Gly	Phe	Ser	Arg
		355					360					365			
Phe	Leu	Lys	Val	Cys	Gly	Ser	Glu	Leu	Val	Arg	Leu	Glu	Leu	Ser	Cys
	370					375					380				
Ser	His	Phe	Leu	Asn	Glu	Thr	Cys	Leu	Glu	Val	Ile	Ser	Glu	Met	Cys
385					390					395					400
Pro	Asn	Leu	Gln	Ala	Leu	Asn	Leu	Ser	Ser	Cys	Asp	Lys	Leu	Pro	Pro
				405					410					415	
Gln	Ala	Phe	Asn	His	Ile	Ala	Lys	Leu	Cys	Ser	Leu	Lys	Arg	Leu	Val
			420					425					430		
Leu	Tyr	Arg	Thr	Lys	Val	Glu	Gln	Thr	Ala	Leu	Leu	Ser	Ile	Leu	Asn
	435						440					445			

Phe Cys Ser Glu Leu Gln His Leu Ser Leu Gly Ser Cys Val Met Ile
 450 455 460
 Glu Asp Tyr Asp Val Ile Ala Ser Met Ile Gly Ala Lys Cys Lys Lys
 465 470 475 480
 Leu Arg Thr Leu Asp Leu Trp Arg Cys Lys Asn Ile Thr Glu Asn Gly
 485 490 495
 Ile Ala Glu Leu Ala Ser Gly Cys Pro Leu Leu Glu Glu Leu Asp Leu
 500 505 510
 Gly Trp Cys Pro Thr Leu Gln Ser Ser Thr Gly Cys Phe Thr Arg Leu
 515 520 525
 Ala His Gln Leu Pro Asn Leu Gln Lys Leu Phe Leu Thr Ala Asn Arg
 530 535 540
 Ser Val Cys Asp Thr Asp Ile Asp Glu Leu Ala Cys Asn Cys Thr Arg
 545 550 555 560
 Leu Gln Gln Leu Asp Ile Leu Gly Thr Arg Met Val Ser Pro Ala Ser
 565 570 575
 Leu Arg Lys Leu Leu Glu Ser Cys Lys Asp Leu Ser Leu Leu Asp Val
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 595 600 605
 Ser Phe Pro Lys Val Phe Ile Lys Lys Ser Phe Thr Gln
 610 615 620

<210> 57
 <211> 984
 <212> DNA
 <213> Homo sapiens

<400> 57
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 tcctacttcc agcagcaact cacatttcag gagtctgtgc ttaaactgtg tcagcctgag 180
 cttgagagca gtcagattca catatcagtg ctgccaatgg aggtcctgat gtacatcttc 240
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 agaggattct acatctgtgc cagagaccct gaaatatggc gtctggcctg cttgaaagt 360
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 cggcctcgtg ttcgggttga tggcgtgtat atcagtaaaa ccacatatat tcgtcaaggg 480
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 gaaaaaccac ttgactataa atacagatat tttcgtcgtg tccctgtaca agaagcagat 780
 cagagttttc atgtggggct acagctatgt tccagtggtc accagaggtt caacaaactc 840
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<210> 58
 <211> 327

<212> PRT

<213> Homo sapiens

<400> 58

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		20					25						30			
Asp	Ser	Lys	Met	Ala	Asp	Leu	Leu	Ser	Tyr	Phe	Gln	Gln	Gln	Leu	Thr	
	35					40					45					
Phe	Gln	Glu	Ser	Val	Leu	Lys	Leu	Cys	Gln	Pro	Glu	Leu	Glu	Ser	Ser	
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Gln	Ile	His	Ile	Ser	Val	Leu	Pro	Met	Glu	Val	Leu	Met	Tyr	Ile	Phe	
65					70				75						80	
					85				90						95	
Ser	Leu	Val	Cys	Arg	Gly	Phe	Tyr	Ile	Cys	Ala	Arg	Asp	Pro	Glu	Ile	
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Val	Pro	Tyr	Thr	Ser	Trp	Arg	Glu	Met	Phe	Leu	Glu	Arg	Pro	Arg	Val	
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Arg	Phe	Asp	Gly	Val	Tyr	Ile	Ser	Lys	Thr	Thr	Tyr	Ile	Arg	Gln	Gly	
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Tyr	Arg	Tyr	Ile	Arg	Phe	Phe	Pro	Asp	Gly	His	Val	Met	Met	Leu	Thr	
		180						185					190			
Thr	Pro	Glu	Glu	Pro	Gln	Ser	Ile	Val	Pro	Arg	Leu	Arg	Thr	Arg	Asn	
	195						200					205				
Thr	Arg	Thr	Asp	Ala	Ile	Leu	Leu	Gly	His	Tyr	Arg	Leu	Ser	Gln	Asp	
	210					215					220					
Thr	Asp	Asn	Gln	Thr	Lys	Val	Phe	Ala	Val	Ile	Thr	Lys	Lys	Lys	Glu	
225					230					235					240	
Glu	Lys	Pro	Leu	Asp	Tyr	Lys	Tyr	Arg	Tyr	Phe	Arg	Arg	Val	Pro	Val	
			245						250					255		
Gln	Glu	Ala	Asp	Gln	Ser	Phe	His	Val	Gly	Leu	Gln	Leu	Cys	Ser	Ser	
		260						265					270			
Gly	His	Gln	Arg	Phe	Asn	Lys	Leu	Ile	Trp	Ile	His	His	Ser	Cys	His	
	275						280					285				
Ile	Thr	Tyr	Lys	Ser	Thr	Gly	Glu	Thr	Ala	Val	Ser	Ala	Phe	Glu	Ile	
	290					295					300					
Asp	Lys	Met	Tyr	Thr	Pro	Leu	Phe	Phe	Ala	Arg	Val	Arg	Ser	Tyr	Thr	

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325

<210> 59
<211> 765
<212> DNA
<213> Homo sapiens

<220>
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<222> all n positions
<223> n=a, c, g or t

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gattctgtag agcgagatat aattttacag tgtagagaag gtgaacttgt acttccggat 180
ttggaaaaag atgatatgat tgttcgccga atcccagcac agaagaaaga agtgccgctg 240
tctggggccc cagatagata ccacccagtc ccttttcccg aaccctggac tcttctcca 300
gaaattcaag caaaatttct ctgtgtactt gaaaggacat gcccattcaa agaaaaaagt 360
aatagctgta gaatattagt tccttcatat cggcagaaga aagatgacat gctgacacgt 420
aagattcagt cctggaaact gggaaactacc gtgcctccca tcagtttcac ncctggcccc 480
tgcatgtagg ctgacttgaa gagatgggag gccatccggg aggccagcag actcaggcac 540
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tccatgagtg atgtcagcgc agaagatgtt caaaacttgc gtcagctgcy ttacgaggag 660
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aaatggaaag atcgtcgaaa aagttacact tcagatctgc agaag 765

<210> 60
<211> 255
<212> PRT
<213> Homo sapiens

<400> 60
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Thr Gly Ala Phe His Ala Asn Pro Tyr Val Leu Arg Ala Phe Glu Asp
20 25 30
Phe Arg Lys Phe Ser Glu Gln Asp Asp Ser Val Glu Arg Asp Ile Ile
35 40 45
Leu Gln Cys Arg Glu Gly Glu Leu Val Leu Pro Asp Leu Glu Lys Asp
50 55 60
Asp Met Ile Val Arg Arg Ile Pro Ala Gln Lys Lys Glu Val Pro Leu
65 70 75 80
Ser Gly Ala Pro Asp Arg Tyr His Pro Val Pro Phe Pro Glu Pro Trp
85 90 95
Thr Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg
100 105 110
Thr Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro
115 120 125

Ser Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser
 130 135 140
 Trp Lys Leu Gly Thr Thr Val Pro Pro Ile Ser Phe Thr Pro Gly Pro
 145 150 155 160
 Cys Ser Glu Ala Asp Leu Lys Arg Trp Glu Ala Ile Arg Glu Ala Ser
 165 170 175
 Arg Leu Arg His Lys Lys Arg Leu Met Val Glu Arg Leu Phe Gln Lys
 180 185 190
 Ile Tyr Gly Glu Asn Gly Ser Lys Ser Met Ser Asp Val Ser Ala Glu
 195 200 205
 Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile
 210 215 220
 Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala
 225 230 235 240
 Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys
 245 250 255

<210> 61
 <211> 36
 <212> PRT
 <213> Homo sapiens

<400> 61
 Leu Pro Pro Glu Leu Ser Phe Thr Ile Leu Ser Tyr Leu Asn Ala Thr
 1 5 10 15
 Asp Leu Cys Leu Ala Ser Cys Val Trp Gln Asp Leu Ala Asn Asp Glu
 20 25 30
 Leu Leu Trp Gln
 35

<210> 62
 <211> 42
 <212> PRT
 <213> Homo sapiens

<400> 62
 Leu Pro Gly Glu Val Leu Glu Tyr Ile Leu Cys Cys Gly Ser Leu Thr
 1 5 10 15
 Ala Ala Asp Ile Gly Arg Val Ser Ser Thr Cys Arg Arg Leu Arg Glu
 20 25 30
 Leu Cys Gln Ser Ser Gly Lys Val Trp Lys
 35 40

<210> 63
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 63

Leu Ala Glu Val Val Glu Arg Val Leu Thr Phe Leu Pro Ala Lys Ala
1 5 10 15

Leu Leu Arg Val Ala Cys Val Cys Arg Leu Trp Arg Glu Cys Val Arg
20 25 30

Arg Val Leu Arg Thr His Arg Ser Val Thr Trp Ile
35 40

<210> 64

<211> 39

<212> PRT

<213> Homo sapiens

<400> 64

Leu Pro Asp Glu Val Val Leu Lys Ile Phe Ser Tyr Leu Leu Glu Gln
1 5 10 15

Asp Leu Cys Arg Ala Ala Cys Val Cys Lys Arg Phe Ser Glu Leu Ala
20 25 30

Asn Asp Pro Asn Leu Trp Lys
35

<210> 65

<211> 41

<212> PRT

<213> Homo sapiens

<400> 65

Leu Pro Leu Glu Leu Trp Arg Met Ile Leu Ala Tyr Leu His Leu Pro
1 5 10 15

Asp Leu Gly Arg Cys Ser Leu Val Cys Arg Ala Trp Tyr Glu Leu Ile
20 25 30

Leu Ser Leu Asp Ser Thr Arg Trp Arg
35 40

<210> 66

<211> 39

<212> PRT

<213> Homo sapiens

<400> 66

Leu Pro Thr Asp Pro Leu Leu Leu Ile Leu Ser Phe Leu Asp Tyr Arg
1 5 10 15

Asp Leu Ile Asn Cys Cys Tyr Val Ser Arg Arg Leu Ser Gln Leu Ser
20 25 30

Ser His Asp Pro Leu Trp Arg
35

<210> 67

<211> 40
<212> PRT
<213> Homo sapiens

<400> 67
Leu Pro Glu Pro Leu Leu Leu Arg Val Leu Ala Ala Leu Pro Ala Ala
1 5 10 15
Glu Leu Val Gln Ala Cys Arg Leu Val Cys Leu Arg Trp Lys Glu Leu
20 25 30
Val Asp Gly Ala Pro Leu Trp Leu
35 40

<210> 68
<211> 40
<212> PRT
<213> Homo sapiens

<400> 68
Leu Phe Pro Pro Glu Leu Val Glu His Ile Ile Ser Phe Leu Pro Val
1 5 10 15
Arg Asp Leu Val Ala Leu Gly Gln Thr Cys Arg Tyr Phe His Glu Val
20 25 30
Cys Asp Gly Glu Gly Val Trp Arg
35 40

<210> 69
<211> 44
<212> PRT
<213> Homo sapiens

<400> 69
Leu Pro Glu Val Leu Leu Leu His Met Cys Ser Tyr Leu Asp Met Arg
1 5 10 15
Ala Leu Gly Arg Leu Ala Gln Val Tyr Arg Trp Leu Trp His Phe Thr
20 25 30
Asn Cys Asp Leu Leu Arg Arg Gln Ile Ala Trp Ala
35 40

<210> 70
<211> 40
<212> PRT
<213> Homo sapiens

<400> 70
Leu Pro Leu His Met Leu Asn Asn Ile Leu Tyr Arg Phe Ser Asp Gly
1 5 10 15
Trp Asp Ile Ile Thr Leu Gly Gln Val Thr Pro Thr Leu Tyr Met Leu
20 25 30
Ser Glu Asp Arg Gln Leu Trp Lys
35 40

<210> 71
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 71
 Leu Pro Asp His Ser Met Val Gln Ile Phe Ser Phe Leu Pro Thr Asn
 1 5 10 15
 Gln Leu Cys Arg Cys Ala Arg Val Cys Arg Arg Trp Tyr Asn Leu Ala
 20 25 30
 Trp Asp Pro Arg Leu Trp Arg
 35

<210> 72
 <211> 44
 <212> PRT
 <213> Homo sapiens

<400> 72
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 1 5 10 15
 Asp Gly Pro Met Pro Phe Leu Gly Arg Ala Ala Arg Val Cys Arg Arg
 20 25 30
 Trp Gln Glu Ala Ala Ser Gln Pro Ala Leu Trp His
 35 40

<210> 73
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 73
 Leu Pro Pro Glu Val Met Leu Ser Ile Phe Ser Tyr Leu Asn Pro Gln
 1 5 10 15
 Glu Leu Cys Arg Cys Ser Gln Val Ser Met Lys Trp Ser Gln Leu Thr
 20 25 30
 Lys Thr Gly Ser Leu Trp Lys
 35

<210> 74
 <211> 39
 <212> PRT
 <213> Homo sapiens

<400> 74
 Leu Pro Lys Glu Leu Leu Leu Arg Ile Phe Ser Phe Leu Asp Ile Val
 1 5 10 15
 Thr Leu Cys Arg Cys Ala Gln Ile Ser Lys Ala Trp Asn Ile Leu Ala
 20 25 30

Leu Asp Gly Ser Asn Trp Gln
35

<210> 75

<211> 48

<212> PRT

<213> Homo sapiens

<400> 75

Leu Pro Tyr Glu Leu Ile Gln Leu Ile Leu Asn His Leu Thr Leu Pro
1 5 10 15

Asp Leu Cys Arg Leu Ala Gln Thr Cys Lys Leu Leu Ser Gln His Cys
20 25 30

Cys Asp Pro Leu Gln Tyr Ile His Leu Asn Leu Gln Pro Tyr Trp Ala
35 40 45

<210> 76

<211> 44

<212> PRT

<213> Homo sapiens

<400> 76

Leu Pro Met Glu Val Leu Met Tyr Ile Phe Arg Trp Val Val Ser Ser
1 5 10 15

Asp Leu Asp Leu Arg Ser Leu Glu Gln Leu Ser Leu Val Cys Arg Gly
20 25 30

Phe Tyr Ile Cys Ala Arg Asp Pro Glu Ile Trp Arg
35 40

<210> 77

<211> 49

<212> PRT

<213> Homo sapiens

<400> 77

Leu Pro Pro Glu Ile Gln Ala Lys Phe Leu Cys Val Leu Glu Arg Thr
1 5 10 15

Cys Pro Ser Lys Glu Lys Ser Asn Ser Cys Arg Ile Leu Val Pro Ser
20 25 30

Tyr Arg Gln Lys Lys Asp Asp Met Leu Thr Arg Lys Ile Gln Ser Trp
35 40 45

Lys

<210> 78

<211> 39

<212> PRT

<213> Homo sapiens

<400> 78

Leu Pro His His Val Val Leu Gln Ile Phe Gln Tyr Leu Pro Leu Leu
1 5 10 15

Asp Arg Ala Cys Ala Ser Ser Val Cys Arg Arg Trp Asn Glu Val Phe
20 25 30

His Ile Ser Asp Leu Trp Arg
35

<210> 79

<211> 43

<212> PRT

<213> Homo sapiens

<400> 79

Leu Trp Ala Trp Gly Glu Lys Gly Val Leu Ser Asn Ile Ser Ala Leu
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Thr Asp Leu Gly Gly Leu Asp Pro Val Trp Leu Val Cys Gly Ser Trp
20 25 30

Arg Arg His Val Gly Ala Gly Leu Cys Trp Ala
35 40

<210> 80

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
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<400> 80

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<210> 81

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
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<400> 81

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<210> 82

<211> 12

<212> PRT

<213> Homo sapiens

<400> 82

Cys Asp Gly Glu Lys Asp Thr Tyr Ser Tyr Leu Ala
1 5 10

<210> 83
<211> 25
<212> PRT
<213> Homo sapiens

<400> 83
Cys Glu Ser Ser Phe Ser Leu Asn Met Asn Phe Ser Ser Lys Arg Thr
1 5 10 15
Lys Phe Lys Ile Thr Thr Ser Met Gln
20 25

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<211> 12
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Pro His Ser